

Figure S1

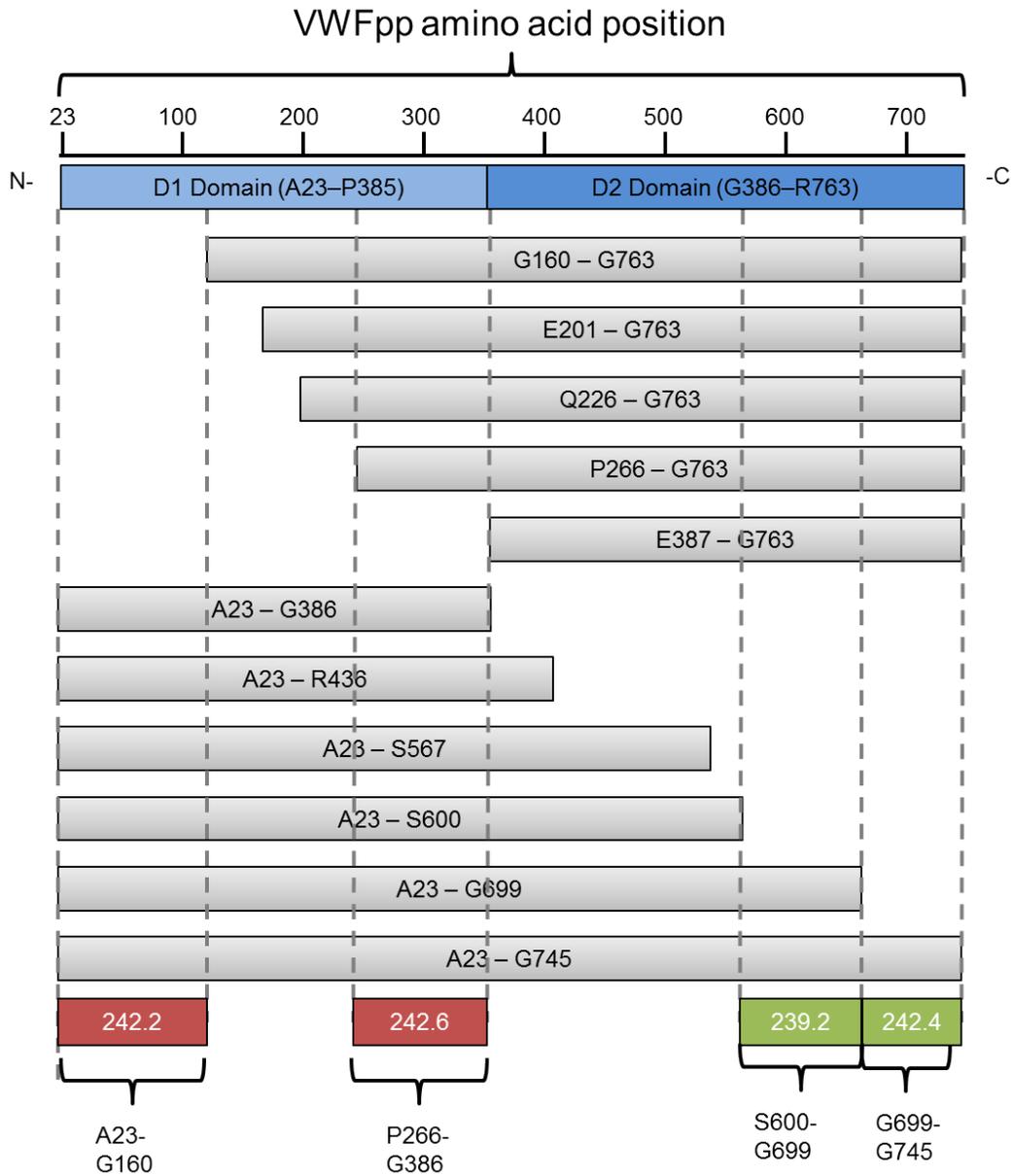


Figure S1. Epitope mapping anti-VWFpp antibodies. Purified VWFpp truncation proteins were used as a target antigen in ELISA. Monoclonal antibodies bound to truncations containing their corresponding epitopes. Minimal binding regions based on ELISA patterns are represented by vertical dotted lines and AlphaLISA antibody pairs are paired by color with anti-D1 pair in red and anti-D2 domain pair in green.

Figure S2

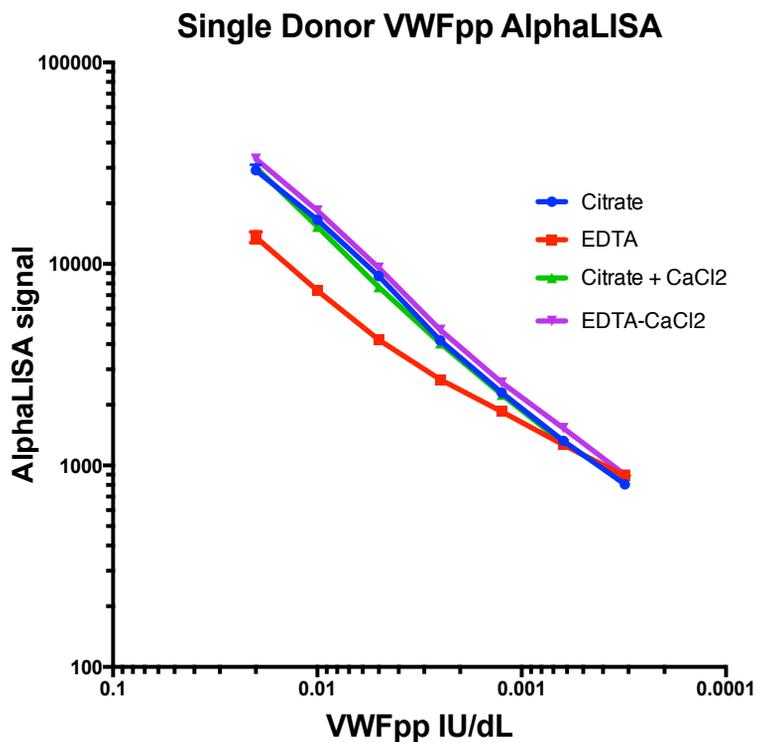
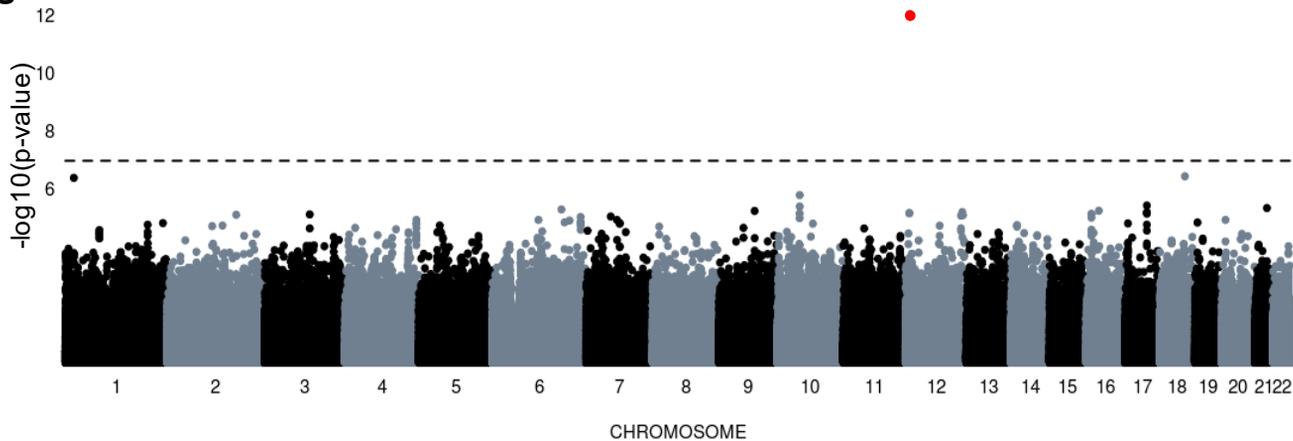


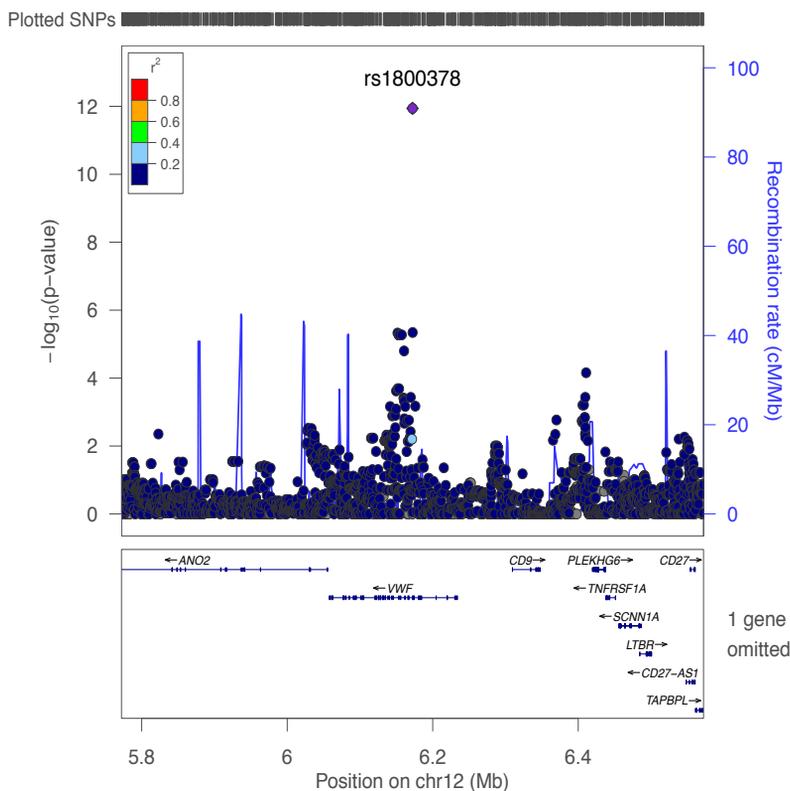
Figure S2. Single Donor VWFpp AlphaLISA Assay. The effects of different anticoagulants (EDTA, citrate) and CaCl₂ (to correct for signal loss associated with the presence of EDTA) used in the sample buffer on the AlphaLISA signal at different concentrations.

Figure S3

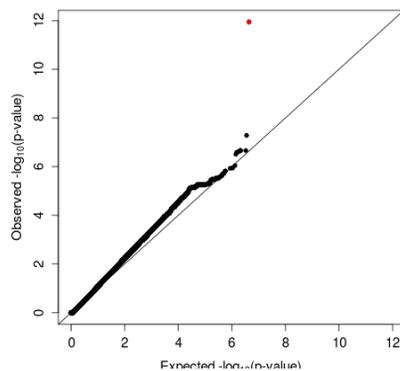
A



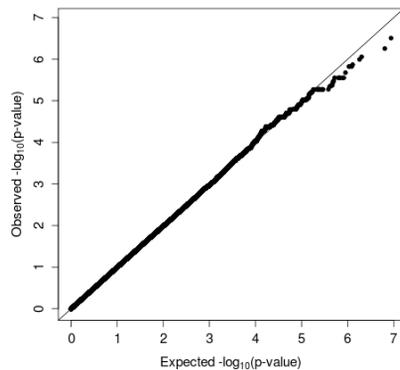
B



C



E



D

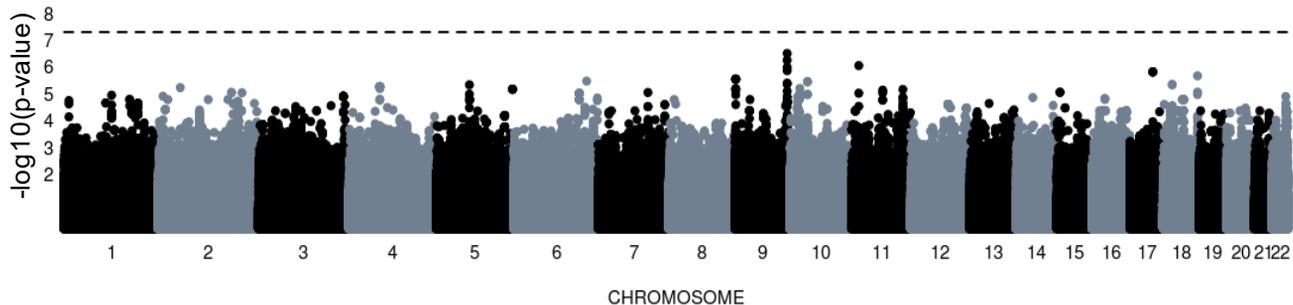


Figure S3. VWFpp association analysis results in GABC. (A) Genome-wide plot of $-\log_{10}(P)$ for ~ 7.29 million imputed SNPs using antio-D2 monoclonal antibodies. The dotted line marks the 5.0×10^{-8} threshold of genome-wide significance. (B) Regional plot for the associated region at the VWF locus on Chr12. (C) Quantile-quantile plot of observed vs. expected $-\log_{10}(P)$ for VWFpp (Anti-D2). SNPs with $-\log_{10}(P) > 7.30$ are shown in red. (D) Genome-wide plot of $-\log_{10}(P)$ for ~ 7.29 million imputed SNPs using anti-D1 monoclonal antibodies. The dotted line marks the 5.0×10^{-8} threshold of genome-wide significance. (E) Quantile-quantile plot of observed vs. expected $-\log_{10}(P)$ for VWFpp (Anti-D1).

Figure S4

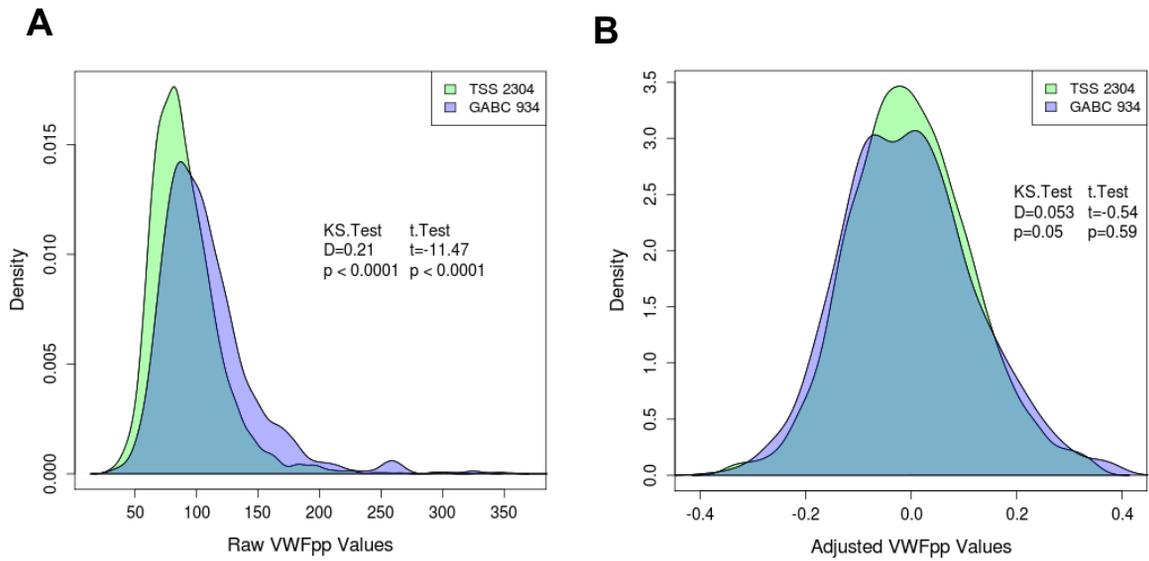
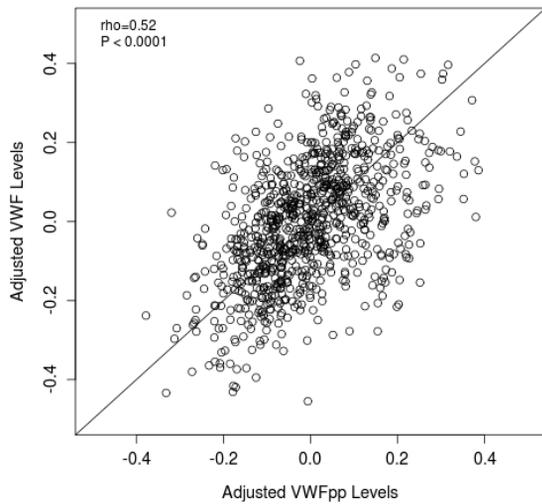


Figure S4. Raw and adjusted VWFpp distributions in the GABC (934 European Individuals) and TSS (2,304 Individuals) Cohorts. (A) Raw VWFpp Levels, (B) Adjusted VWFpp levels. Between-cohort differences are tested by K-S test and t-test.

Figure S5

A



B

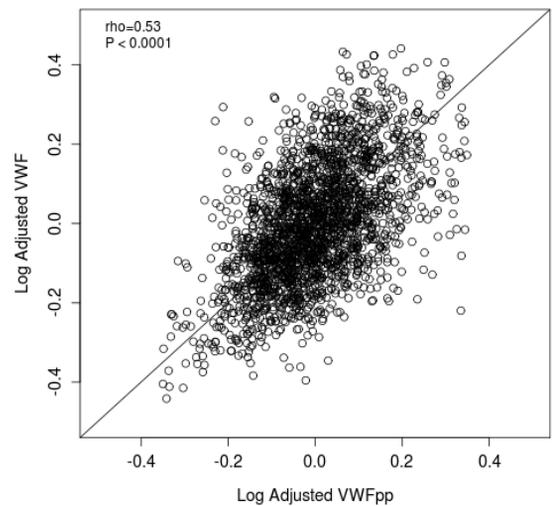


Figure S5. Scatter plot of individual log adjusted VWFpp and VWF levels of the (A) GABC and (B) TSS study participants. Spearman's rho and P values are indicated in upper left.

Figure S6

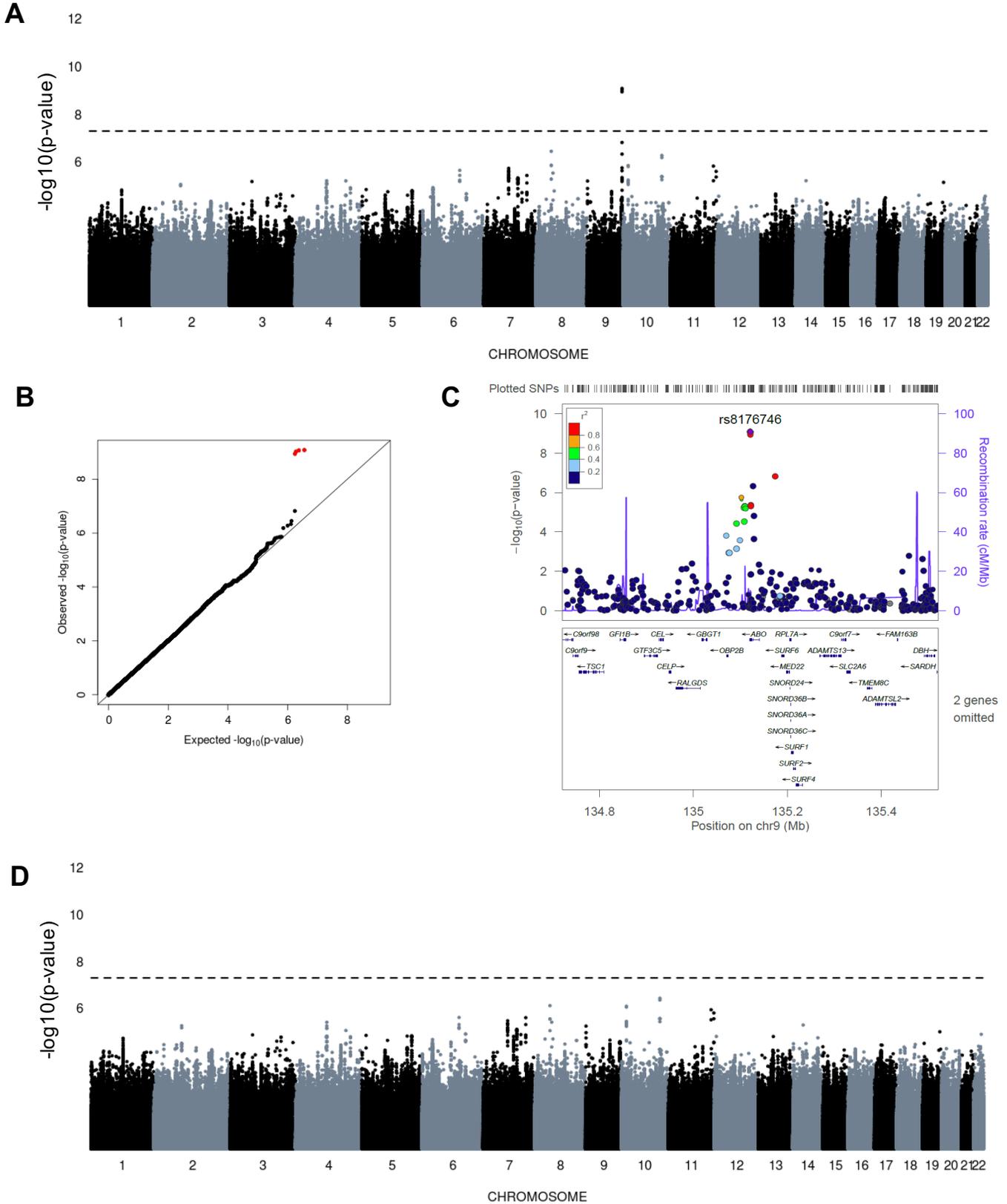


Figure S6. VWFpp association analysis results in TSS. (A) Genome-wide plot of $-\log_{10}(P)$ for ~ 3.7 million imputed SNPs. The dotted line marks the 5.0×10^{-8} threshold of genome-wide significance. (B) Quantile-quantile plot of observed vs. expected $-\log_{10}(P)$ for VWFpp. SNPs with $-\log_{10}(P) > 7.30$ are shown in red. (C) Regional plot for the associated region at the ABO locus on Chr9q34. (D) Conditional analysis using the top SNP (rs8176746).

Figure S7

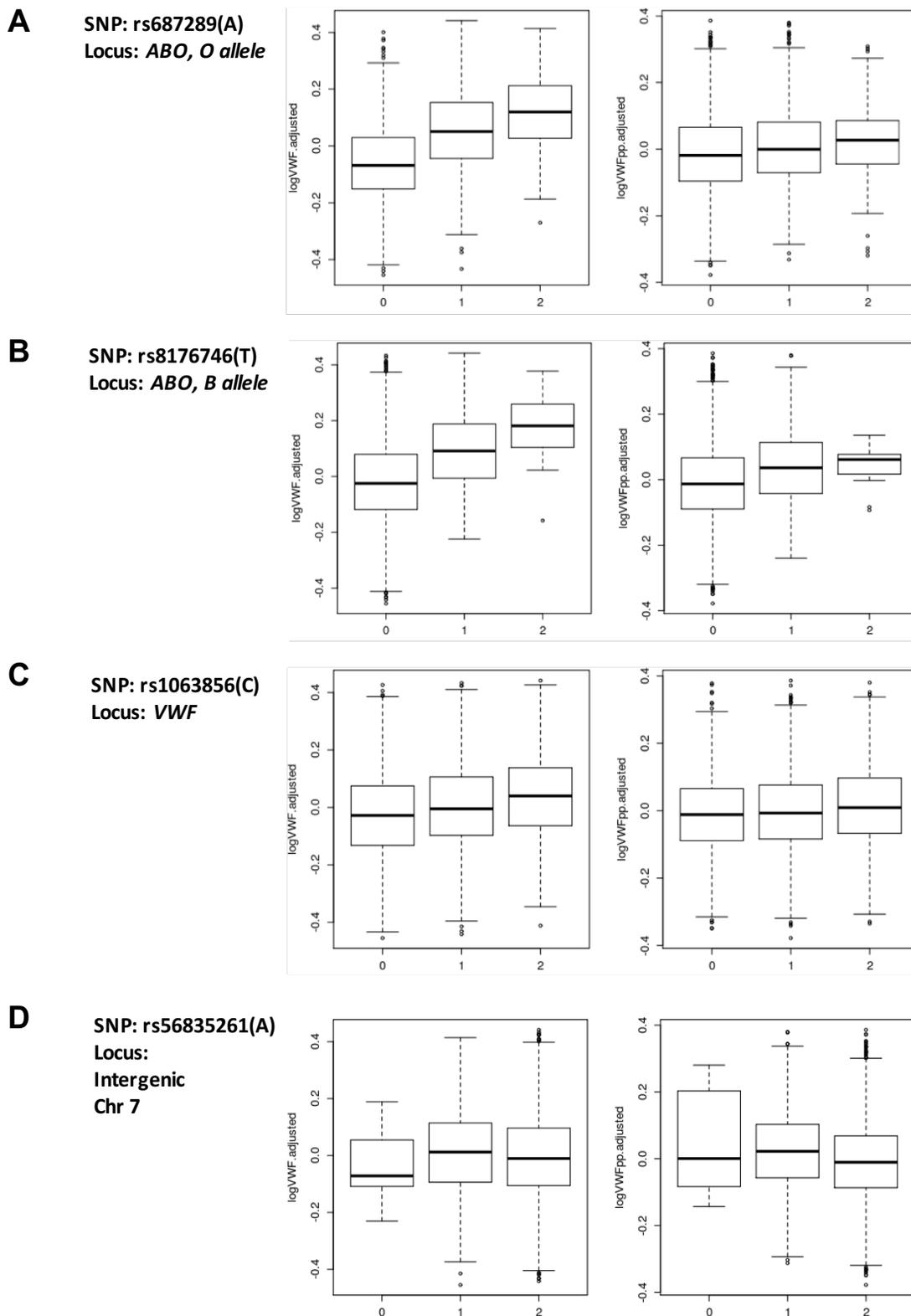


Figure S7. Distribution of log transformed VWF and VWFpp by top meta-analysis SNP allelic series. Boxplot distributions of log transformed and covariate adjusted VWF and VWFpp levels in the combined GABC and TSS cohorts (N=3,238). The numbers 0, 1, 2 on the X axis refer to the number of minor alleles so that 0 is homozygous major allele (indicated by the base pair in parentheses after the SNP rs number), 1 is heterozygous and 2 is homozygous minor allele. A: rs687289(A) where the major allele encodes the ABO O. B: rs8176746(T) where the minor allele tags the ABO B. C: rs1063856(C) D: rs56835261(A)